What is claimed is:

1.(Currently Amended) A method of identifying ~~one or more markers~~ a marker useful for detecting diabetes, said method ~~wherein each of said one or more markers corresponds to a gene transcript,~~ comprising ~~the steps of~~:

a) using an oligonucleotide of predetermined sequence, detecting a presence in RNA of blood samples which have not been fractionated into cell types from subjects having diabetes, of RNA encoded by a gene, said gene expressed in blood and in a non-blood tissue of a subject not having diabetes, said oligonucleotide being specific only for RNA, or cDNA complementary to said RNA, encoded by said gene in said samples, ~~determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having diabetes, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for diabetes; and~~

b) quantifying a level of said RNA encoded by said gene; and ~~comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals not having diabetes,~~

c) determining a difference between said quantified level and a quantified level of a control RNA encoded by said gene in RNA of blood samples which have not been fractionated into cell types from control subjects, said control RNA having been detected in said samples from said control subjects,

thereby identifying said gene as being a marker useful for detecting diabetes.

~~wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being markers for diabetes~~.

2. (Currently Amended) A method of identifying two ~~one~~ or more markers useful for detecting diabetes, said method ~~wherein each of said one or more markers corresponds to a gene transcript,~~ comprising ~~the steps of~~:

for each of a collection of two or more genes;

a) using an oligonucleotide of predetermined sequence, detecting a presence in

RNA of blood samples which have not been fractionated into cell types from subjects having diabetes, of RNA encoded by said gene, said oligonucleotide being specific only for RNA, or cDNA complementary to said RNA, encoded by said gene in said samples, said gene being expressed in blood and in a non-blood tissue of a subject not having diabetes; ~~determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having diabetes, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for diabetes; and~~

b) quantifying a level of said RNA encoded by said gene; and ~~comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals having diabetes,~~

c) determining a difference between said quantified level and a quantified level of control RNA encoded by said gene in RNA of blood samples which have not been fractionated into cell types from control subjects, said control RNA having been detected in said samples from said control subjects,

thereby identifying said two or more genes as two or more markers useful in detecting diabetes.

~~wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being markers for diabetes.~~

3.(currently amended) A method of identifying ~~one or more markers of a stage of~~ a marker useful for detecting diabetes, said method comprising: ~~diabetes progression or regression, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:~~

a) producing amplification products from RNA of blood samples which have not been fractionated into cell types, from subjects having diabetes, using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by a gene in said samples, said gene being expressed in blood and in a non-blood tissue of a subject not having diabetes; ~~determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of diabetes, wherein said one or more individuals are at the same~~

~~progressive or regressive stage of diabetes, and wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for determining the stage of progression or regression of diabetes, and~~;

b) quantifying a level of said amplification products; and ~~comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of diabetes distinct from that of said one or more individuals of step a),~~

c) determining a difference between said quantified level of said amplification products and a quantified level of amplification products produced using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene from control RNA, in RNA of blood samples which have not been fractionated into cell types, said control RNA having been detected in said samples from said control subjects,

thereby identifying said gene as being a marker useful for detecting diabetes.

~~wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being markers for the stage of progression or regression of diabetes.~~

4.(currently amended) A method of identifying two ~~one~~ or more markers ~~of a stage of diabetes progression or regression, wherein each of said one or more markers corresponds to a gene transcript,~~ useful for detecting diabetes, said method comprising ~~the steps of~~:

for each of a collection of two or more genes;

a) producing amplification products from RNA of blood samples which have not been fractionated into cell types from subjects having diabetes, using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene of said subjects, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having diabetes; ~~, said determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of diabetes, wherein said one or more individuals are at the same progressive or regressive stage of diabetes, and wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for determining the stage of progression or regression of diabetes, and;~~

b) quantifying a level of said amplification products; and ~~comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of diabetes identical to that of said one or more individuals of step a),~~

c) Determining a difference between said quantified level of said amplification products and a quantified level of amplification products produced using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene, from control RNA in RNA of blood samples which have not been fractionated into cell types, from control subjects, said control RNA having been detected in said samples from said control subjects,

thereby identifying said collection of said two or more genes as two or more markers useful for detecting diabetes.

~~wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being markers for the stage of progression or regression of diabetes.~~

5. (currently amended) The method of any one of claims 1-4, wherein each of said one or more markers ~~identifies one or more transcripts of one or more~~ corresponds to a non immune response genes.

6. (canceled)

7. (currently amended) The method of any one of claims 1-4, wherein each of said one or more markers corresponds to a gene expressed ~~identifies a transcript of a gene expressed~~ by non-lymphoid tissue.

8. (original) The method of any one of claims 1-4, wherein said diabetes is either symptomatic or asymptomatic.

9. (currently amended) The method of any one of claims 1-4, ~~claim 8~~ wherein said diabetes is type II diabetes.

10. (original) The method of any one of claims 1-4, wherein said one or more markers identifies one or more genes selected from the group of genes listed in Table 3G.

11. (canceled)

12. (currently amended) A method of detecting a difference in expression of a gene in a human test subject as compared with human control subjects, said method comprising: ~~diagnosing or prognosing diabetes in an individual, comprising the steps of:~~

a) using an oligonucleotide of predetermined sequence, detecting in RNA of a blood sample from said test subject which has not been fractionated into cell types, RNA encoded by said gene in said sample, wherein said gene is expressed in blood and in a non-blood tissue in a subject who is not said test subject, said oligonucleotide being specific only for RNA or cDNA complementary to said RNA, encoded by said gene; ~~determining the level of one or more gene transcripts in blood obtained from said individual, wherein said one or more gene transcripts corresponds to said one or more markers of claim 1 and claim 2, and~~

b) quantifying a level of said RNA encoded by said gene; and ~~comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having diabetes,~~

c)determining a difference between said level and a quantified level of control RNA encoded by said gene in RNA of blood samples which have not been fractionated into cell types from said control subjects, wherein said difference is indicative of diabetes in said test subject,

thereby detecting a difference in expression of said gene in said human test subject vs. said human control subjects.

~~wherein detecting a difference in the levels of each of said one or more gene transcripts in the comparison of step b) is indicative of diabetes in the individual of step a).~~

13. (currently amended) A method of detecting a difference in expression of each of two or more genes of human test subjects vs. human control subjects; ~~diagnosing or prognosing diabetes in an individual, comprising the steps of:~~

a) using an oligonucleotide of predetermined sequence, detecting in RNA of a blood sample from said test subject which has not been fractionated into cell types, RNA encoded by said gene in said sample, wherein said gene is expressed in blood and in a non-blood tissue in a subject who is not said test subject, said oligonucleotide being specific only for RNA, or cDNA complementary to said

RNA, encoded by said gene; ~~determining the level of one or more gene transcripts in blood obtained from said individual, wherein said one or more gene transcripts corresponds to said one or more markers of claim 1 and claim 2,~~ and

b) quantifying a level of said amplification product; and ~~comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having diabetes~~,

c) determining a difference between said level and a quantified level of control RNA encoded by said gene in RNA of blood samples which have not been fractionated into cell types from said one or more control subjects, said control RNA having been detected in said samples for said control subjects; wherein said difference for each said gene is indicative of diabetes in said test subject,

thereby detecting a difference in expression of each said gene in said collection of two or more genes in blood of said human test subjects vs. said human control subjects.

~~wherein detecting the same levels of each of said one or more gene transcripts in the comparison of step b) is indicative of diabetes in the individual of step a).~~

14. (currently amended) A method of detecting a difference in expression of a gene of a human test subject vs. human control subjects, said method ~~determining a stage of disease progression or regression in an individual having diabetes,~~ comprising ~~the steps of~~:

a) producing amplification products from RNA of a blood sample from said test subject which has not been fractionated into cell types, using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene, wherein said gene is expressed in blood and in a non-blood tissue of a subject who is not said test subject; ~~determining the level of one or more gene transcripts in blood obtained from said individual having diabetes, wherein said one or more gene transcripts corresponds to said one or more markers of claim 3 and claim 4, and~~

b) quantifying a level of said amplification product; and ~~comparing the level of each if said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood obtained from one or more individuals who each have been diagnosed as being at the same~~

~~progressive or regressive stage of diabetes,~~

c) determining a difference between said quantified level of said amplification products and a quantified level of amplification products produced using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene, applied to control RNA of blood samples which have not been fractionated into cell types from said control subjects, wherein detection of said difference for said gene is indicative of diabetes in said test subject,

thereby detecting a difference in expression of each said gene in said collection of two or more genes in blood of said human test subjects vs. said human control subjects.

~~wherein the comparison from step b) allows the determination of the stage of diabetes progression or regression in an individual.~~

15. (Currently amended) A method of ~~diagnosing or prognosing diabetes in an individual, comprising the steps of:~~ detecting a difference in expression of each of two or more genes of a human test subject vs. human control subjects, said method comprising:

for each gene of said collection of two or more genes:

a) producing an amplification product from RNA of a blood sample from said test subject which has not been fractionated into cell types, using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene, wherein said gene is expressed in blood and in a non-blood tissue of a subject who is not said test subject; and ~~determining the level of one or more gene transcripts expressed in blood obtained from said individual, wherein said one or more gene transcripts corresponds to said one or more markers of claim 3 and claim 4,~~ and

b) quantifying a level of said amplification product, ~~comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having diabetes,~~

c) determining a difference between said quantified level of said amplification product and a quantified level of amplification products produced using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene applied to control RNA of blood samples which have not been

fractionated into cell types from said control subjects, said control RNA having been detected in said samples from said control subjects, wherein determining a difference for each said gene is indicative of diabetes in said test subject,

~~comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having diabetes~~

~~d) determining whether the level of said one or more gene transcripts of step a) are characterized as classifying with the levels of said transcripts in step b) as compared with levels of said transcripts in step c),~~

thereby detecting a difference in expression of each said gene in said collection of two or more genes in blood of said human test subjects vs. said human control subjects.

~~wherein said determination is indicative of said individual of step a) having diabetes.~~

16. (canceled)

17.(currently amended) The method of any one of claims 12-15~~12-16~~, wherein each of said ~~one or more markers~~ genes is ~~identifies a transcript of a gene~~ selected from the ~~group consisting of the~~ genes listed in Table 3G.

18.(canceled)

19.(currently amended) The method of any one of claims12-15~~12-16~~, wherein said diabetes is either symptomatic or asymptomatic.

20.(currently amended) The method of any one of claims 12-15 ~~1-4 and 12-16~~, wherein said diabetes is type II diabetes.

21.-24. (canceled)

25. (currently amended)The method of any one of claims 1-4 and 12-15, ~~21,~~ further comprising the step of isolating RNA from said ~~blood~~ samples.

26. (currently amended)The method of any one of claims 1-2 and 12-15, ~~1-4 and 12-16~~, wherein ~~the step~~ said steps of determining said levels of RNA encoded b said gene in step (a) and/or step (b) is effected using ~~the level of each of said one or more gene transcripts comprises~~ quantitative RT-PCR (QRT-PCR)~~, wherein said one or more transcripts are from step a) and/or step b) of claims 1-4 and 12-16~~.

27.(Canceled)

28.(Currently amended) The method of any one of claims 1-4 and 12-15, ~~claim 27,~~ wherein said primers are 15-25 nucleotides in length.

29.(Canceled)

30.(Currently amended) The method of any one of claims 1-4 and 12-15, wherein the step of determining said levels of RNA encoded by each of said genes in step (a) and/or step (b) is by ~~the level of each of said one or more gene transcripts comprises~~ hybridizing a first plurality of isolated nucleic acid molecules that correspond to said genes ~~one or more transcripts,~~ to an array comprising a second plurality of isolated nucleic acid molecules.

31.(original) The method of claim 30, wherein said first plurality of isolated nucleic acid molecules comprises RNA, DNA, cDNA, PCR products or ESTs.

32.(original) The method of claim 30, wherein said array comprises a plurality of isolated nucleic acid molecules comprising RNA, DNA, cDNA, PCR products or ESTs.

33.(Canceled)

34.(original) The method of claim 32, wherein said array comprises two or more of the markers of claim 2.

35 .(original) The method of claim 32, wherein said array comprises two or more of the markers of claim 3.

36 .(original) The method of claim 32, wherein said array comprises two or more of the markers of claim 4.

37 .(original) The method of claim 32, wherein said array comprises a plurality of nucleic acid molecules that correspond to genes of the human genome.

38. (original) The method of claim 32, wherein said array comprises a plurality of nucleic acid molecules that correspond to two or more sequences of two or more genes selected from the group of genes listed in Table 3G.

39. (original) A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 1.

40. (original) A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 2.

41. (original) A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 3.

42. (original) A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 4.

43.(canceled)

44. (original) An array consisting essentially of the plurality of nucleic acid molecules of claim 39.

45. (original) An array consisting essentially of the plurality of nucleic acid molecules of claim 40.

46. (original) An array consisting essentially of the plurality of nucleic acid molecules of claim 41.

47. (original) An array consisting essentially of the plurality of nucleic acid molecules of claim 42.

48. (original) A kit for diagnosing or prognosing diabetes comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene that corresponds to a marker selected from the group consisting of markers of claim 1, claim 2, claim 3, and claim 4; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity;

c) an enzyme with thermostable DNA polymerase activity; and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

49. (original) A kit for monitoring a course of therapeutic treatment of diabetes, comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene that corresponds to a marker selected from the group consisting of markers of claim 1, claim 2, claim 3, and claim 4; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity;

c) an enzyme with thermostable DNA polymerase activity; and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

50. (original) A kit for monitoring progression or regression of diabetes, comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene that corresponds to a marker selected from the group consisting of markers of claim 1, claim 2, claim 3, and claim 4; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity;

c) an enzyme with thermostable DNA polymerase activity; and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

51. (original) The kit of any one of claims 48 to 50 wherein said gene-specific priming means identified in step a) is selected from the group of genes listed in Table 3G.

52. (original) A plurality of nucleic acid molecules that identify or correspond to two or more sequences of two or more genes selected from the group of genes listed in Table 3G.

53.(canceled)

54. (new) The method of any of claims 1-4 wherein none of said control subjects have diabetes.

55. (new) The method of any of claims 1-4 wherein said control subjects have diabetes at a different stage than said subjects having diabetes.

56. (new)A method of identifying a marker useful for detecting diabetes, said method comprising:

a) using an oligonucleotide of predetermined sequence, detecting a presence in RNA of unfractionated cells of a lysed blood sample from subjects having diabetes, of RNA encoded by a gene, said gene expressed in blood and in a non-blood tissue of a subject not having diabetes, said oligonucleotide being specific only for RNA, or cDNA complementary to said RNA, encoded by said gene in said samples,

b) quantifying a level of said RNA encoded by said gene; and

c) determining a difference between said quantified level and a quantified level of a control RNA encoded by said gene in RNA of unfractionated cells of a lysed blood sample from control subjects, said control RNA having been detected in said samples from said control subjects,

thereby identifying said gene as being a marker useful for detecting diabetes.

57. (new)A method of identifying two or more markers useful for detecting diabetes, said method comprising:

for each of a collection of two or more genes

a) using an oligonucleotide of predetermined sequence, detecting a presence in RNA of unfractionated cells of a lysed blood sample from subjects having diabetes of RNA encoded by said gene, said oligonucleotide being specific only for RNA, or cDNA complementary to said RNA, encoded by said gene in said samples, said gene being expressed in blood and in a non-blood tissue of a subject not having diabetes;

b) quantifying a level of said RNA encoded by said gene; and

c) determining a difference between said quantified level and a quantified level of control RNA encoded by said gene in RNA of unfractionated cells of a lysed blood sample from control subjects, said control RNA having been detected in said samples from said control subjects,

thereby identifying said two or more genes as two or more markers useful in detecting diabetes.

58. (new) A method of identifying a marker useful for detecting diabetes, said method comprising:

a) producing amplification products from RNA of unfractionated cells of a lysed blood sample, from subjects having diabetes, using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by a gene in said samples, said gene being expressed in blood and in a non-blood tissue of a subject not having diabetes;

b) quantifying a level of said amplification products; and

c) determining a difference between said quantified level of said amplification products and a quantified level of amplification products produced using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene from control RNA, in RNA of unfractionated cells of a lysed blood sample, said control RNA having been detected in said samples from said control subjects,

thereby identifying said gene as being a marker useful for detecting diabetes.

59. (new)A method of identifying two or more markers useful for detecting diabetes said method comprising:

for each of a collection of two or more genes:

a) producing amplification products from RNA of unfractionated cells of a lysed blood sample from subjects having diabetes, using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene of said subjects, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having diabetes;

b) quantifying a level of said amplification products; and

c) Determining a difference between said quantified level of said amplification products and a quantified level of amplification products produced using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene, from control RNA in RNA of unfractionated cells of a lysed blood sample, from control subjects, said control RNA having been detected in said samples from said control subjects,

thereby identifying said collection of said two or more genes as two or more markers useful for detecting diabetes.

60. (new)A method of detecting a difference in expression of a gene in a human test subject as compared with human control subjects, said method comprising:

a) using an oligonucleotide of predetermined sequence, detecting in RNA of a unfractionated cells of a lysed blood sample of said test subject, RNA encoded by said gene in said sample, wherein said gene is expressed in blood and in a non-blood tissue in a subject who is not said test subject, said oligonucleotide being specific only for RNA or cDNA complementary to said RNA, encoded by said gene;

b) quantifying a level of said RNA encoded by said gene; and

c) determining a difference between said level and a quantified level of control RNA encoded by said gene in RNA of unfractionated cells of a lysed blood sample from said control subjects, wherein said difference is indicative of diabetes in said test subject,

thereby detecting a difference in expression of said gene in said human test subject vs. said human control subjects.

61. (new) A method of detecting a difference in expression of each of two or more genes of a human test subjects vs. human control subjects:
for each gene of a collection of said two or more genes:

a) using an oligonucleotide of predetermined sequence, detecting in RNA of a unfractionated cells of a lysed blood sample from said test subject, RNA encoded by said gene in said sample, wherein said gene is expressed in blood and in a non-blood tissue in a subject who is not said test subject, said oligonucleotide being specific only for RNA, or cDNA complementary to said RNA, encoded by said gene;

b) quantifying a level of said RNA encoded by said gene; and

c) determining a difference between said level and a quantified level of control RNA encoded by said gene in RNA of unfractionated cells of a lysed blood sample from said control subjects, said control RNA having been detected in said samples for said control

subjects; wherein said difference for each said gene is indicative of diabetes in said test subject,

thereby detecting a difference in expression of each said gene in said collection of two or more genes in blood of said human test subjects vs. said human control subjects.

62. (new) A method of detecting a difference in expression of a gene of a human test subject vs. human control subjects, said method comprising:

a) producing amplification products from RNA of a blood sample unfractionated cells of a lysed blood sample from said test subject, using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene, wherein said gene is expressed in blood and in a non-blood tissue of a subject who is not said test subject;

b) quantifying a level of said amplification product; and

c) determining a difference between said quantified level of said amplification products and a quantified level of amplification products produced using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene, applied to control RNA of unfractionated cells of a lysed blood sample from said control subjects, wherein detection of said difference for said gene is indicative of diabetes in said test subject,

thereby detecting a difference in expression of said gene in blood of said human test subject vs. human control subjects.

63. (New) A method of detecting a difference in expression of each of two or more genes of a human test subject vs. human control subjects, said method comprising:

for each gene of said collection of two or more genes:

a) producing an amplification product from RNA of a unfractionated cells of a lysed blood sample from said test subject, using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene, wherein said gene is expressed in blood and in a non-blood tissue of a subject who is not said test subject; and

b) quantifying a level of said amplification product,

c) determining a difference between said quantified level of said amplification product and a quantified level of amplification products produced using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene applied to control

RNA of unfractionated cells of a lysed blood sample from said control subjects, said control RNA having been detected in said samples from said control subjects, wherein detecting a difference for each said gene is indicative of diabetes in said test subject,

thereby detecting a difference in expression of each said gene in said collection of two or more genes in blood of said human test subjects vs. said human control subjects.

64. (New) A method for detecting diabetes in a human test subject, comprising:

a) Quantifying in RNA of a blood sample from said test subject, a level of RNA encoded by the gene DAZ interacting protein 1 (DZIP1) in said sample; and

b) Comparing said quantified level with a quantified level of control RNA encoded by said gene in RNA of blood samples from control subjects;

wherein said comparison of said quantified level of step (a) with said quantified level of said control RNA is indicative of diabetes in said human test subject.

65. (New) The method of claim 49, wherein said blood sample of step (a) and said blood samples from said control subjects in step (b) have not been fractionated into cell types.

66. (New) The method of claim 49, wherein said blood sample of step (a) and said blood samples from said control subjects in step (b) are unfractionated samples of lysed blood.

67. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is effected by quantifying said RNA relative to a housekeeping gene.

68. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is effected by quantification of cDNA corresponding to said RNA.

69. (New) The method of any of claims 49, 50 or 51, wherein said control subjects do not have diabetes and said comparison of step (b) results in a statistically significant difference.

70. (New) The method of any of claims 49, 50 or 51, wherein said control subjects have been diagnosed as having diabetes and said comparison results in a statistically significant similarity.

71. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is determined using quantitative real-time RT-PCR.

72. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is determined using an array.